

## SEQUENCE LISTING

5 SEQ ID NO: 1 is mouse TECK nucleotide sequence.  
SEQ ID NO: 2 is mouse TECK amino acid sequence.  
SEQ ID NO: 3 is human TECK nucleotide sequence.  
SEQ ID NO: 4 is human TECK amino acid sequence.  
SEQ ID NO: 5 is human MIP-3 $\alpha$  nucleotide sequence.  
SEQ ID NO: 6 is human MIP-3 $\alpha$  amino acid sequence.  
10 SEQ ID NO: 7 is human MIP-3 $\beta$  nucleotide sequence.  
SEQ ID NO: 8 is human MIP-3 $\beta$  amino acid sequence.  
SEQ ID NO: 9 is human DC CR nucleotide sequence.  
SEQ ID NO: 10 is human DC CR amino acid sequence.  
SEQ ID NO: 11 is human M/DC CR nucleotide sequence.  
15 SEQ ID NO: 12 is human M/DC CR amino acid sequence.  
SEQ ID NO: 13 is human CCKR1 amino acid sequence.  
SEQ ID NO: 14 is human CCKR2 amino acid sequence.  
SEQ ID NO: 15 is human CCKR3 amino acid sequence.  
SEQ ID NO: 16 is human CCKR4 amino acid sequence.  
20 SEQ ID NO: 17 is HPRT sense primer.  
SEQ ID NO: 18 is HPRT antisense primer.  
SEQ ID NO: 19 is FLAG epitope tag sequence.

25 (1) GENERAL INFORMATION:

(i) APPLICANT: Wang, Wei  
Gish, Kurt C.  
Schall, Thomas J.  
30 Vicari, Alain P.  
Zlotnik, Albert

(ii) TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS

35 (iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: DNAX Research Institute  
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40 (C) CITY: Palo Alto  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94304-1104

45 (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
50

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:  
55

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/675,814  
(B) FILING DATE: 05-JUL-1996  
60

provisional filings DX0589P, DX0589P1; DX0589P2

various

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ching, Edwin P.  
(B) REGISTRATION NUMBER: 34,090  
(C) REFERENCE/DOCKET NUMBER: DX0589Q1

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-852-9196  
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## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1034 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 94..525

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

30 AGGCTACAAG CAGGCACCAG CTCTCAGGAC CAGAAAGGCA TTGGTGGCCC CCTTAAACCT 60  
TCAGGTATCT GGAGAGGAGA TCTAACCTTC ACT ATG AAA CTG TGG CTT TTT GCC 114  
Met Lys Leu Trp Leu Phe Ala  
1 5  
35 TGC CTG GTT GCC TGT TTT GTT GGG GCC TGG ATG CCG GTT GTC CAT GCC 162  
Cys Leu Val Ala Cys Phe Val Gly Ala Trp Met Pro Val Val His Ala  
10 15 20  
40 CAA GGT GCC TTT GAA GAC TGC TGC CTG GGT TAC CAG CAC AGG ATC AAA 210  
Gln Gly Ala Phe Glu Asp Cys Cys Leu Gly Tyr Gln His Arg Ile Lys  
25 30 35  
45 TGG AAT GTT CTC CGG CAT GCT AGG AAT TAT CAC CAG CAG GAA GTG AGT 258  
Trp Asn Val Leu Arg His Ala Arg Asn Tyr His Gln Gln Glu Val Ser  
40 45 50 55  
50 GGA AGC TGC AAC CTA CGT GCT GTG AGA TTC TAC TTC CGC CAG AAA GTA 306  
Gly Ser Cys Asn Leu Arg Ala Val Arg Phe Tyr Phe Arg Gln Lys Val  
60 65 70  
GTG TGT GGG AAT CCA GAG GAC ATG AAT GTG AAG AGG GCG ATA AGA ATC 354  
Val Cys Gly Asn Pro Glu Asp Met Asn Val Lys Arg Ala Ile Arg Ile  
75 80 85  
55 TTG ACA GCT AGG AAA AGG CTA GTC CAC TGG AAG AGC GCC TCA GAC TCT 402  
Leu Thr Ala Arg Lys Arg Leu Val His Trp Lys Ser Ala Ser Asp Ser  
90 95 100  
60 CAG ACT GAA AGG AAG AAG TCA AAC CAT ATG AAG TCC AAG GTG GAG AAC 450

Gln Thr Glu Arg Lys Lys Ser Asn His Met Lys Ser Lys Val Glu Asn  
 105 110 115

5 CCC AAC AGT ACA AGC GTG AGG AGT GCC ACC CTA GGT CAT CCC AGG ATG 498  
 Pro Asn Ser Thr Ser Val Arg Ser Ala Thr Leu Gly His Pro Arg Met  
 120 125 130 135

10 GTG ATG ATG CCC AGA AAG ACC AAC AAT TAAGTTAATT ACTCAGAGTA 545  
 Val Met Met Pro Arg Lys Thr Asn Asn  
 140

15 AGCACCAGCT GGAGGATGGG CGGAGTCTGC TGAAGTGCTG TCTTCTAGGC ATGCCAGTGC 605  
 CAATGAACTC ACTGAAGCTA CAGTTTCCTG TACAAGACCA GACCCACCAA CGTCTCAGCA 665  
 TGTACGAGGA AGGAACTACT GCGCTAAAGG CCCTCCCACT CACCAAGGAG CTATTGGCTA 725  
 TTGATGATTG CTGAGGGAAG GGAGTAATTT TTTTCTCTT TCTGAAGTGT GACTTGAGTA 785

20 AATTGCCCAT AGTTCAGTAT ATAATCCCCA ACCTGTGCTC AGGCAAGCAA CCCTAATTAA 845  
 ATGCAATAGC CACATACAAA AGAAGAGGAT ATGAATAGTT TGGTAGGAGG GGCTTGTTAG 905  
 25 GAAGAAGACA TTAACAGGAG AGAGAGGAGC GAGAGGATAG TGAGTGTGTG AGAGTGCCTG 965  
 CACGTGTGAA ATGGTCAAAG AATTAAAAA TAAAACTTA AAAAGCTATT AAAAAGTAAA 1025  
 AAAAATAAAA 1034

30 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 144 amino acids  
 35 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Leu Trp Leu Phe Ala Cys Leu Val Ala Cys Phe Val Gly Ala  
 1 5 10 15

45 Trp Met Pro Val Val His Ala Gln Gly Ala Phe Glu Asp Cys Cys Leu  
 20 25 30

Gly Tyr Gln His Arg Ile Lys Trp Asn Val Leu Arg His Ala Arg Asn  
 35 40 45

50 Tyr His Gln Gln Glu Val Ser Gly Ser Cys Asn Leu Arg Ala Val Arg  
 50 55 60

55 Phe Tyr Phe Arg Gln Lys Val Val Cys Gly Asn Pro Glu Asp Met Asn  
 65 70 75 80

Val Lys Arg Ala Ile Arg Ile Leu Thr Ala Arg Lys Arg Leu Val His  
 85 90 95

60 Trp Lys Ser Ala Ser Asp Ser Gln Thr Glu Arg Lys Lys Ser Asn His

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          100          105          110
Met Lys Ser Lys Val Glu Asn Pro Asn Ser Thr Ser Val Arg Ser Ala
      115          120          125
5  Thr Leu Gly His Pro Arg Met Val Met Met Pro Arg Lys Thr Asn Asn
      130          135          140

10  (2) INFORMATION FOR SEQ ID NO:3:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1012 base pairs
            (B) TYPE: nucleic acid
15      (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: cDNA

20      (ix) FEATURE:
            (A) NAME/KEY: CDS
            (B) LOCATION: 117..566

25      (ix) FEATURE:
            (A) NAME/KEY: mat_peptide
            (B) LOCATION: 186..566

30      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGACCCACG CGTCCGCTTG GCCTACAGCC CGGCGGGCAT CAGCTCCCTT GACCCAGTGG      60
ATATCGGTGG CCCCGTTATT CGTCCAGGTG CCCAGGGAGG AGGACCCGCC TGCAGC      116
35  ATG AAC CTG TGG CTC CTG GCC TGC CTG GTG GCC GGC TTC CTG GGA GCC      164
Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala
-23          -20          -15          -10
40  TGG GCC CCC GCT GTC CAC ACC CAA GGT GTC TTT GAG GAC TGC TGC CTG      212
Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu
-5          1          5
45  GCC TAC CAC TAC CCC ATT GGG TGG GCT GTG CTC CGG CGC GCC TGG ACT      260
Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr
10          15          20          25
50  TAC CGG ATC CAG GAG GTG AGC GGG AGC TGC AAT CTG CCT GCT GCG ATA      308
Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile
30          35          40
55  TTC TAC CTC CCC AAG AGA CAC AGG AAG GTG TGT GGG AAC CCC AAA AGC      356
Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser
45          50          55
60  AGG GAG GTG CAG AGA GCC ATG AAG CTC CTG GAT GCT CGA AAT AAG GTT      404
Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val
60          65          70
60  TTT GCA AAG CTC CAC CAC AAC ATG CAG ACC TTC CAA GCA GGC CCT CAT      452

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Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His  
 75 80 85  
 5 GCT GTA AAG AAG TTG AGT TCT GGA AAC TCC AAG TTA TCA TCA TCC AAG 500  
 Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys  
 90 95 100 105  
 10 TTT AGC AAT CCC ATC AGC AGC AGC AAG AGG AAT GTC TCC CTC CTG ATA 548  
 Phe Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile  
 110 115 120  
 TCA GCT AAT TCA GGA CTG TGAGCCGGCT CATTTCTGGG CTCCATCGGC 596  
 Ser Ala Asn Ser Gly Leu  
 125  
 15 ACAGGAGGGG CCGGATCTTT CTCCGATAAA ACCGTCGCCC TACAGACCCA GCTGTCCCCA 656  
 CGCCTCTGTC TTTTGGGTCA AGTCTTAATC CCTGCACCTG AGTTGGTCCT CCCTCTGCAC 716  
 20 CCCCACCACC TCCTGCCCCG CTGGCAACTG GAAAGAAGGA GTTGGCCTGA TTTTAACCTT 776  
 TTGCCGCTCC GGGGAACAGC ACAATCCTGG GCAGCCAGTG GCTCTTGTAG AGAAACTTA 836  
 GGATACCTCT CTCACCTTCT GTTTCTTGCC GTCCACCCCG GGCCATGCCA GTGTGTCCTC 896  
 25 TGGGTCCCCT CCAAAAATCT GGTCATTCAA GGATCCCCTC CCAAGGCTAT GCTTTTCTAT 956  
 AACTTTTAAA TAAACCTTGG GGGGTGAATG GAATAAAAAA AAAAAAAAAA AAAAAA 1012  
 30  
 (2) INFORMATION FOR SEQ ID NO:4:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 150 amino acids  
 35 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
 Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala  
 -23 -20 -15 -10  
 45 Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu  
 -5 1 5  
 Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr  
 10 15 20 25  
 50 Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile  
 30 35 40  
 Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser  
 55 45 50 55  
 Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val  
 60 65 70  
 60 Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His

75 80 85

Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys  
 90 95 100 105

5 Phe Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile  
 110 115 120

Ser Ala Asn Ser Gly Leu  
 10 125

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
 15 (A) LENGTH: 801 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA  
 20

(ix) FEATURE:  
 25 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..288

(ix) FEATURE:  
 30 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 79..288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG TGC TGT ACC AAG AGT TTG CTC CTG GCT GCT TTG ATG TCA GTG CTG 48  
 35 Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu  
 -26 -25 -20 -15

CTA CTC CAC CTC TGC GGC GAA TCA GAA GCA GCA AGC AAC TTT GAC TGC 96  
 40 Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys  
 -10 -5 1 5

TGT CTT GGA TAC ACA GAC CGT ATT CTT CAT CCT AAA TTT ATT GTG GGC 144  
 Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly  
 10 15 20

TTC ACA CGG CAG CTG GCC AAT GAA GGC TGT GAC ATC AAT GCT ATC ATC 192  
 Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile  
 25 30 35

TTT CAC ACA AAG AAA AAG TTG TCT GTG TGC GCA AAT CCA AAA CAG ACT 240  
 50 Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr  
 40 45 50

TGG GTG AAA TAT ATT GTG CGT CTC CTC AGT AAA AAA GTC AAG AAC ATG 288  
 55 Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met  
 55 60 65 70

TAAAACTGT GGCTTTTCTG GAATGGAATT GGACATAGCC CAAGAACAGA AAGAACCTTG 348

60 CTGGGGTTGG AGGTTTCACT TGCACATCAT GGAGGGTTTA GTGCTTATCT AATTTGTGCC 408

5 TCACTGGACT TGTCCAATTA ATGAAGTTGA TTCATATTGC ATCATAGTTT GCTTTGTTTA 468  
AGCATCACAT TAAAGTTAAA CTGTATTTTA TGTTATTTAT AGCTGTAGGT TTTCTGTGTT 528  
TAGCTATTTA AATAAATTT TCCATAAGCT ATTTTGTTT AGTGCAAAGT ATAAAATTAT 588  
ATTTGGGGGG GAATAAGATT ATATGGACTT TTTTGCAAGC AACAAGCTAT TTTTAAAAA 648  
10 AACTATTTA ACATTCTTTT GTTTATATTG TTTTGTCTCC TAAATTGTTG TAATTGCATT 708  
ATAAAATAAG AAAAATATTA ATAAGACAAA TATTGAAAAAT AAAGAAACAA AAAGTTAAAA 768  
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA 801  
15

## (2) INFORMATION FOR SEQ ID NO:6:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 96 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
  
25 (ii) MOLECULE TYPE: protein  
  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
  
Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu  
-26 -25 -20 -15  
30 Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys  
-10 -5 1 5  
Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly  
35 10 15 20  
Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile  
25 30 35  
40 Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr  
40 45 50  
Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met  
45 55 60 65 70

## (2) INFORMATION FOR SEQ ID NO:7:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 699 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
  
55 (ii) MOLECULE TYPE: cDNA  
  
(ix) FEATURE:  
(A) NAME/KEY: CDS  
60 (B) LOCATION: 142..435

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

5 GGCACGAGCG GCACGAGCAT CACTCACACC TTGCATTTCA CCCCTGCATC CCAGTCGCCC 60  
 TGCAGCCTCA CACAGATCCT GCACACACCC AGACAGCTGG CGCTCACACA TTCACCGTTG 120  
 GCCTGCCTCT GTTCACCCTC C ATG GCC CTG CTA CTG GCC CTC AGC CTG CTG 171  
 10 Met Ala Leu Leu Leu Ala Leu Ser Leu Leu  
 1 5 10  
 GTT CTC TGG ACT TCC CCA GCC CCA ACT CTG AGT GGC ACC AAT GAT GCT 219  
 15 Val Leu Trp Thr Ser Pro Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala  
 15 20 25  
 GAA GAC TGC TGC CTG TCT GTG ACC CAG AAA CCC ATC CCT GGG TAC ATC 267  
 Glu Asp Cys Cys Leu Ser Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile  
 30 35 40  
 20 GTG AGG AAC TTC CAC TAC CTT CTC ATC AAG GAT GGC TGC AGG GTG CCT 315  
 Val Arg Asn Phe His Tyr Leu Leu Ile Lys Asp Gly Cys Arg Val Pro  
 45 50 55  
 25 GCT GTA GTG TTC ACC ACA CTG AGG GGC CGC CAG CTC TGT GCA CCC CCA 363  
 Ala Val Val Phe Thr Thr Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro  
 60 65 70  
 GAC CAG CCC TGG GTA GAA CGC ATC ATC CAG AGA CTG CAG AGG ACC TCA 411  
 30 Asp Gln Pro Trp Val Glu Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser  
 75 80 85 90  
 GCC AAG ATG AAG CGC CGC AGC AGT TAACCTATGA CCGTGCAGAG GGAGCCCGGA 465  
 35 Ala Lys Met Lys Arg Arg Ser Ser  
 95  
 GTCCGAGTCA AGCATTGTGA ATTATTACCT AACCTGGGGA ACCGAGGACC AGAAGGAAGG 525  
 ACCAGGCTTC CAGCTCCTCT GCACCAGACC TGACCAGCCA GGACAGGGCC TGGGGTGTGT 585  
 40 GTGAGTGTGA GTGTGAGCGA GAGGGTGAGT GTGGTCTAGA GTAAAGCTGC TCCACCCCCA 645  
 GATTGCAATG CTACCAATAA AGCCGCCTGG TGTTTACAAC TAAAAA AAAA 699

45

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 98 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Leu Leu Leu Ala Leu Ser Leu Leu Val Leu Trp Thr Ser Pro  
 1 5 10 15  
 60 Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala Glu Asp Cys Cys Leu Ser

20 25 30

Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val Arg Asn Phe His Tyr  
35 40 45

5 Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr  
50 55 60

10 Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Glu  
65 70 75 80

Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser Ala Lys Met Lys Arg Arg  
85 90 95

15 Ser Ser

## (2) INFORMATION FOR SEQ ID NO:9:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1119 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA

30 (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..1095

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TTT TCG ACT CCA GTG AAG ATT ATT TTG TGT CAG TCA ATA CTT CAT 48  
Met Phe Ser Thr Pro Val Lys Ile Ile Leu Cys Gln Ser Ile Leu His  
1 5 10 15

40 ATT ACT CAG TTG ATT CTG AGA TGT TAC TGT GCT CCT TGC AGG AGG TCA 96  
Ile Thr Gln Leu Ile Leu Arg Cys Tyr Cys Ala Pro Cys Arg Arg Ser  
20 25 30

45 GGC AGT TCT CCA GGC TAT TTG TAC CGA ATT GCC TAC TCC TTG ATC TGT 144  
Gly Ser Ser Pro Gly Tyr Leu Tyr Arg Ile Ala Tyr Ser Leu Ile Cys  
35 40 45

50 GTT CTT GGC CTC CTG GGG AAT ATT CTG GTG GTG ATC ACC TTT GCT TTT 192  
Val Leu Gly Leu Leu Gly Asn Ile Leu Val Val Ile Thr Phe Ala Phe  
50 55 60

55 TAT AAG AAG GCC AGG TCT ATG ACA GAC GTC TAT CTC TTG AAC ATG GCC 240  
Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala  
65 70 75 80

ATT GCA GAC ATC CTC TTT GTT CTT ACT CTC CCA TTC TGG GCA GTG AGT 288  
Ile Ala Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Ser  
85 90 95

60 CAT GCC ACT GGT GCG TGG GTT TTC AGC AAT GCC ACG TGC AAG TTG CTA 336

	His	Ala	Thr	Gly	Ala	Trp	Val	Phe	Ser	Asn	Ala	Thr	Cys	Lys	Leu	Leu	
				100					105					110			
5	AAA	GGC	ATC	TAT	GCC	ATC	AAC	TTT	AAC	TGC	GGG	ATG	CTG	CTC	CTG	ACT	384
	Lys	Gly	Ile	Tyr	Ala	Ile	Asn	Phe	Asn	Cys	Gly	Met	Leu	Leu	Leu	Thr	
			115					120					125				
10	TGC	ATT	AGC	ATG	GAC	CGG	TAC	ATC	GCC	ATT	GTA	CAG	GCG	ACT	AAG	TCA	432
	Cys	Ile	Ser	Met	Asp	Arg	Tyr	Ile	Ala	Ile	Val	Gln	Ala	Thr	Lys	Ser	
			130				135					140					
15	TTC	CGG	CTC	CGA	TCC	AGA	ACA	CTA	CCG	CGC	AGC	AAA	ATC	ATC	TGC	CTT	480
	Phe	Arg	Leu	Arg	Ser	Arg	Thr	Leu	Pro	Arg	Ser	Lys	Ile	Ile	Cys	Leu	
	145					150					155					160	
20	GTT	GTG	TGG	GGG	CTG	TCA	GTC	ATC	ATC	TCC	AGC	TCA	ACT	TTT	GTC	TTC	528
	Val	Val	Trp	Gly	Leu	Ser	Val	Ile	Ile	Ser	Ser	Ser	Thr	Phe	Val	Phe	
					165					170					175		
25	AAC	CAA	AAA	TAC	AAC	ACC	CAA	GGC	AGC	GAT	GTC	TGT	GAA	CCC	AAG	TAC	576
	Asn	Gln	Lys	Tyr	Asn	Thr	Gln	Gly	Ser	Asp	Val	Cys	Glu	Pro	Lys	Tyr	
				180					185					190			
30	CAA	ACT	GTC	TCG	GAG	CCC	ATC	AGG	TGG	AAG	CTG	CTG	ATG	TTG	GGG	CTT	624
	Gln	Thr	Val	Ser	Glu	Pro	Ile	Arg	Trp	Lys	Leu	Leu	Met	Leu	Gly	Leu	
			195					200					205				
35	GAG	CTA	CTC	TTT	GGT	TTC	TTT	ATC	CCT	TTG	ATG	TTC	ATG	ATA	TTT	TGT	672
	Glu	Leu	Leu	Phe	Gly	Phe	Phe	Ile	Pro	Leu	Met	Phe	Met	Ile	Phe	Cys	
		210					215					220					
40	TAC	ACG	TTC	ATT	GTC	AAA	ACC	TTG	GTG	CAA	GCT	CAG	AAT	TCT	AAA	AGG	720
	Tyr	Thr	Phe	Ile	Val	Lys	Thr	Leu	Val	Gln	Ala	Gln	Asn	Ser	Lys	Arg	
	225					230				235						240	
45	CAC	AAA	GCC	ATC	CGT	GTA	ATC	ATA	GCT	GTG	GTG	CTT	GTG	TTT	CTG	GCT	768
	His	Lys	Ala	Ile	Arg	Val	Ile	Ile	Ala	Val	Val	Leu	Val	Phe	Leu	Ala	
					245					250					255		
50	TGT	CAG	ATT	CCT	CAT	AAC	ATG	GTC	CTG	CTT	GTG	ACG	GCT	GCT	AAT	TTG	816
	Cys	Gln	Ile	Pro	His	Asn	Met	Val	Leu	Leu	Val	Thr	Ala	Ala	Asn	Leu	
				260				265							270		
55	GGT	AAA	ATG	AAC	CGA	TCC	TGC	CAG	AGC	GAA	AAG	CTA	ATT	GGC	TAT	ACG	864
	Gly	Lys	Met	Asn	Arg	Ser	Cys	Gln	Ser	Glu	Lys	Leu	Ile	Gly	Tyr	Thr	
			275					280					285				
60	AAA	ACT	GTC	ACA	GAA	GTC	CTG	GCT	TTC	CTG	CAC	TGC	TGC	CTG	AAC	CCT	912
	Lys	Thr	Val	Thr	Glu	Val	Leu	Ala	Phe	Leu	His	Cys	Cys	Leu	Asn	Pro	
			290				295					300					
65	GTG	CTC	TAC	GCT	TTT	ATT	GGG	CAG	AAG	TTC	AGA	AAC	TAC	TTT	CTG	AAG	960
	Val	Leu	Tyr	Ala	Phe	Ile	Gly	Gln	Lys	Phe	Arg	Asn	Tyr	Phe	Leu	Lys	
	305					310					315					320	
70	ATC	TTG	AAG	GAC	CTG	TGG	TGT	GTG	AGA	AGG	AAG	TAC	AAG	TCC	TCA	GGC	1008
	Ile	Leu	Lys	Asp	Leu	Trp	Cys	Val	Arg	Arg	Lys	Tyr	Lys	Ser	Ser	Gly	
					325					330					335		
75	TTC	TCC	TGT	GCC	GGG	AGG	TAC	TCA	GAA	AAC	ATT	TCT	CGG	CAG	ACC	AGT	1056

Phe Ser Cys Ala Gly Arg Tyr Ser Glu Asn Ile Ser Arg Gln Thr Ser  
 340 345 350

5 GAG ACC GCA GAT AAC GAC AAT GCG TCG TCC TTC ACT ATG TGATAGAAAG 1105  
 Glu Thr Ala Asp Asn Asp Asn Ala Ser Ser Phe Thr Met  
 355 360 365

CTGAGTCTCC CTAA 1119

10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 365 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Phe Ser Thr Pro Val Lys Ile Ile Leu Cys Gln Ser Ile Leu His  
 1 5 10 15

25 Ile Thr Gln Leu Ile Leu Arg Cys Tyr Cys Ala Pro Cys Arg Arg Ser  
 20 25 30

Gly Ser Ser Pro Gly Tyr Leu Tyr Arg Ile Ala Tyr Ser Leu Ile Cys  
 35 40 45

30 Val Leu Gly Leu Leu Gly Asn Ile Leu Val Val Ile Thr Phe Ala Phe  
 50 55 60

35 Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala  
 65 70 75 80

Ile Ala Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Ser  
 85 90 95

40 His Ala Thr Gly Ala Trp Val Phe Ser Asn Ala Thr Cys Lys Leu Leu  
 100 105 110

Lys Gly Ile Tyr Ala Ile Asn Phe Asn Cys Gly Met Leu Leu Leu Thr  
 115 120 125

45 Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser  
 130 135 140

50 Phe Arg Leu Arg Ser Arg Thr Leu Pro Arg Ser Lys Ile Ile Cys Leu  
 145 150 155 160

Val Val Trp Gly Leu Ser Val Ile Ile Ser Ser Ser Thr Phe Val Phe  
 165 170 175

55 Asn Gln Lys Tyr Asn Thr Gln Gly Ser Asp Val Cys Glu Pro Lys Tyr  
 180 185 190

Gln Thr Val Ser Glu Pro Ile Arg Trp Lys Leu Leu Met Leu Gly Leu  
 195 200 205

60

Glu Leu Leu Phe Gly Phe Phe Ile Pro Leu Met Phe Met Ile Phe Cys  
 210 215 220  
 Tyr Thr Phe Ile Val Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg  
 225 230 235 240  
 His Lys Ala Ile Arg Val Ile Ile Ala Val Val Leu Val Phe Leu Ala  
 245 250 255  
 Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Ala Asn Leu  
 260 265 270  
 Gly Lys Met Asn Arg Ser Cys Gln Ser Glu Lys Leu Ile Gly Tyr Thr  
 275 280 285  
 Lys Thr Val Thr Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro  
 290 295 300  
 Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe Leu Lys  
 305 310 315 320  
 Ile Leu Lys Asp Leu Trp Cys Val Arg Arg Lys Tyr Lys Ser Ser Gly  
 325 330 335  
 Phe Ser Cys Ala Gly Arg Tyr Ser Glu Asn Ile Ser Arg Gln Thr Ser  
 340 345 350  
 Glu Thr Ala Asp Asn Asp Asn Ala Ser Ser Phe Thr Met  
 355 360 365

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1547 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 49..1116

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGGAAGCTG CTTGGGGGGG TGAGCAAAC TTTTAAATG CAGAAATT ATG ATC TAC 57  
 Met Ile Tyr  
 1  
 ACC CGT TTC TTA AAA GGC AGT CTG AAG ATG GCC AAT TAC ACG CTG GCA 105  
 Thr Arg Phe Leu Lys Gly Ser Leu Lys Met Ala Asn Tyr Thr Leu Ala  
 5 10 15  
 CCA GAG GAT GAA TAT GAT GTC CTC ATA GAA GGT GAA CTG GAG AGC GAT 153  
 Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu Glu Ser Asp  
 20 25 30 35

	GAG	GCA	GAG	CAA	TGT	GAC	AAG	TAT	GAC	GCC	CAG	GCA	CTC	TCA	GCC	CAG	201
	Glu	Ala	Glu	Gln	Cys	Asp	Lys	Tyr	Asp	Ala	Gln	Ala	Leu	Ser	Ala	Gln	
					40					45					50		
5	CTG	GTG	CCA	TCA	CTC	TGC	TCT	GCT	GTG	TTT	GTG	ATC	GGT	GTC	CTG	GAC	249
	Leu	Val	Pro	Ser	Leu	Cys	Ser	Ala	Val	Phe	Val	Ile	Gly	Val	Leu	Asp	
				55					60					65			
10	AAT	CTC	CTG	GTT	GTG	CTT	ATC	CTG	GTA	AAA	TAT	AAA	GGA	CTC	AAA	CGC	297
	Asn	Leu	Leu	Val	Val	Leu	Ile	Leu	Val	Lys	Tyr	Lys	Gly	Leu	Lys	Arg	
			70					75					80				
15	GTG	GAA	AAT	ATC	TAT	CTT	CTA	AAC	TTG	GCA	GTT	TCT	AAC	TTG	TGT	TTC	345
	Val	Glu	Asn	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Val	Ser	Asn	Leu	Cys	Phe	
		85					90					95					
20	TTG	CTT	ACC	CTG	CCC	TTC	TGG	GCT	CAT	GCT	GGG	GGC	GAT	CCC	ATG	TGT	393
	Leu	Leu	Thr	Leu	Pro	Phe	Trp	Ala	His	Ala	Gly	Gly	Asp	Pro	Met	Cys	
	100					105					110					115	
	AAA	ATT	CTC	ATT	GGA	CTG	TAC	TTC	GTG	GGC	CTG	TAC	AGT	GAG	ACA	TTT	441
	Lys	Ile	Leu	Ile	Gly	Leu	Tyr	Phe	Val	Gly	Leu	Tyr	Ser	Glu	Thr	Phe	
					120					125					130		
25	TTC	AAT	TGC	CTT	CTG	ACT	GTG	CAA	AGG	TAC	CTA	GTG	TTT	TTG	CAC	AAG	489
	Phe	Asn	Cys	Leu	Leu	Thr	Val	Gln	Arg	Tyr	Leu	Val	Phe	Leu	His	Lys	
				135				140						145			
30	GGC	AAC	TTT	TTC	TCA	GCC	AGG	AGG	AGG	GTG	CCC	TGT	GGC	ATC	ATT	ACA	537
	Gly	Asn	Phe	Phe	Ser	Ala	Arg	Arg	Arg	Val	Pro	Cys	Gly	Ile	Ile	Thr	
			150				155						160				
35	AGT	GTC	CTG	GCA	TGG	GTA	ACA	GCC	ATT	CTG	GCC	ACT	TTG	CCT	GAA	TTC	585
	Ser	Val	Leu	Ala	Trp	Val	Thr	Ala	Ile	Leu	Ala	Thr	Leu	Pro	Glu	Phe	
		165				170						175					
40	GTG	GTT	TAT	AAA	CCT	CAG	ATG	GAA	GAC	CAG	AAA	TAC	AAG	TGT	GCA	TTT	633
	Val	Val	Tyr	Lys	Pro	Gln	Met	Glu	Asp	Gln	Lys	Tyr	Lys	Cys	Ala	Phe	
	180					185					190					195	
	AGC	AGA	ACT	CCC	TTC	CTG	CCA	GCT	GAT	GAG	ACA	TTC	TGG	AAG	CAT	TTT	681
	Ser	Arg	Thr	Pro	Phe	Leu	Pro	Ala	Asp	Glu	Thr	Phe	Trp	Lys	His	Phe	
				200						205					210		
45	CTG	ACT	TTA	AAA	ATG	AAC	ATT	TCG	GTT	CTT	GTC	CTC	CCC	CTA	TTT	ATT	729
	Leu	Thr	Leu	Lys	Met	Asn	Ile	Ser	Val	Leu	Val	Leu	Pro	Leu	Phe	Ile	
				215				220						225			
50	TTT	ACA	TTT	CTC	TAT	GTG	CAA	ATG	AGA	AAA	ACA	CTA	AGG	TTC	AGG	GAG	777
	Phe	Thr	Phe	Leu	Tyr	Val	Gln	Met	Arg	Lys	Thr	Leu	Arg	Phe	Arg	Glu	
			230				235						240				
55	CAG	AGG	TAT	AGC	CTT	TTC	AAG	CTT	GTT	TTT	GCC	GTA	ATG	GTA	GTC	TTC	825
	Gln	Arg	Tyr	Ser	Leu	Phe	Lys	Leu	Val	Phe	Ala	Val	Met	Val	Val	Phe	
		245					250					255					
60	CTT	CTG	ATG	TGG	GCG	CCC	TAC	AAT	ATT	GCA	TTT	TTC	CTG	TCC	ACT	TTC	873
	Leu	Leu	Met	Trp	Ala	Pro	Tyr	Asn	Ile	Ala	Phe	Phe	Leu	Ser	Thr	Phe	
	260					265					270					275	

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AAA GAA CAC TTC TCC CTG AGT GAC TGC AAG AGC AGC TAC AAT CTG GAC      921
Lys Glu His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr Asn Leu Asp
                      280                      285                      290

5  AAA AGT GTT CAC ATC ACT AAA CTC ATC GCC ACC ACC CAC TGC TGC ATC      969
   Lys Ser Val His Ile Thr Lys Leu Ile Ala Thr Thr His Cys Cys Ile
                      295                      300                      305

10 AAC CCT CTC CTG TAT GCG TTT CTT GAT GGG ACA TTT AGC AAA TAC CTC      1017
   Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser Lys Tyr Leu
                      310                      315                      320

15 TGC CGC TGT TTC CAT CTG CGT AGT AAC ACC CCA CTT CAA CCC AGG GGG      1065
   Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln Pro Arg Gly
                      325                      330                      335

20 CAG TCT GCA CAA GGC ACA TCG AGG GAA GAA CCT GAC CAT TCC ACC GAA      1113
   Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His Ser Thr Glu
   340                      345                      350                      355

   GTG TAAACTAGCA TCCACCAAAT GCAAGAAGAA TAAACATGGA TTTTCATCTT      1166
   Val

25 TCTGCATTAT TTCATGTAAA TTTTCTACAC ATTTGTATAC AAAATCGGAT ACAGGAAGAA      1226

   AAGGGAGAGG TGAGCTAACA TTTGCTAAGC ACTGAATTTG TCTCAGGCAC CGTGCAAGGC      1286

30 TCTTTACAAA CGTGAGCTCC TTCGCCCTCCT ACCACTTGTC CATAGTGTGG ATAGGACTAG      1346
   TCTCATTTCT CTGAGAAGAA AACTAAGGCG CGGAAATTTG TCTAAGATCA CATAACTAGG      1406
   AAGTGGCAGA ACTGATTCTC CAGCCCTGGT AGCATTTGCT CAGAGCCTAC GCTTGGTCCA      1466

35 GAACATCAAA CTCCAAACCC TGGGGACAAA CGACATGAAA TAAATGTATT TTAAACATA      1526
   TAAAAAAAAA AAAAAAAAAA A      1547

40 (2) INFORMATION FOR SEQ ID NO:12:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 356 amino acids
            (B) TYPE: amino acid
45      (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

50 Met Ile Tyr Thr Arg Phe Leu Lys Gly Ser Leu Lys Met Ala Asn Tyr
   1                      5                      10                      15

   Thr Leu Ala Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu
55                      20                      25                      30

   Glu Ser Asp Glu Ala Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu
                      35                      40                      45

60 Ser Ala Gln Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly

```

	50	55	60
	Val Leu Asp Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly		
	65	70	75 80
5	Leu Lys Arg Val Glu Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn		
		85 90	95
10	Leu Cys Phe Leu Leu Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp		
		100 105	110
	Pro Met Cys Lys Ile Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser		
		115 120	125
15	Glu Thr Phe Phe Asn Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe		
		130 135	140
	Leu His Lys Gly Asn Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly		
		145 150	155 160
20	Ile Ile Thr Ser Val Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu		
		165 170	175
	Pro Glu Phe Val Val Tyr Lys Pro Gln Met Glu Asp Gln Lys Tyr Lys		
		180 185	190
25	Cys Ala Phe Ser Arg Thr Pro Phe Leu Pro Ala Asp Glu Thr Phe Trp		
		195 200	205
30	Lys His Phe Leu Thr Leu Lys Met Asn Ile Ser Val Leu Val Leu Pro		
		210 215	220
	Leu Phe Ile Phe Thr Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg		
		225 230	235 240
35	Phe Arg Glu Gln Arg Tyr Ser Leu Phe Lys Leu Val Phe Ala Val Met		
		245 250	255
	Val Val Phe Leu Leu Met Trp Ala Pro Tyr Asn Ile Ala Phe Phe Leu		
		260 265	270
40	Ser Thr Phe Lys Glu His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr		
		275 280	285
45	Asn Leu Asp Lys Ser Val His Ile Thr Lys Leu Ile Ala Thr Thr His		
		290 295	300
	Cys Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser		
		305 310	315 320
50	Lys Tyr Leu Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln		
		325 330	335
	Pro Arg Gly Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His		
		340 345	350
55	Ser Thr Glu Val		
		355	

60 (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 355 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

15 Met Glu Thr Pro Asn Thr Thr Glu Asp Tyr Asp Thr Thr Thr Glu Phe  
 1 5 10 15  
 20 Asp Tyr Gly Asp Ala Thr Pro Cys Gln Lys Val Asn Glu Arg Ala Phe  
 20 20 25 30  
 25 Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Val Ile Gly  
 35 40 45  
 30 Leu Val Gly Asn Ile Leu Val Val Leu Val Leu Val Gln Tyr Lys Arg  
 50 55 60  
 35 Leu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp  
 65 70 75 80  
 40 Leu Leu Phe Leu Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys  
 85 90 95  
 45 Asp Asp Trp Val Phe Gly Asp Ala Met Cys Lys Ile Leu Ser Gly Phe  
 100 105 110  
 50 Tyr Tyr Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr  
 115 120 125  
 55 Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala  
 130 135 140  
 60 Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Ile Ile Trp Ala Leu  
 145 150 155 160  
 65 Ala Ile Leu Ala Ser Met Pro Gly Leu Tyr Phe Ser Lys Thr Gln Trp  
 165 170 175  
 70 Glu Phe Thr His His Thr Cys Ser Leu His Phe Pro His Glu Ser Leu  
 180 185 190  
 75 Arg Glu Trp Lys Leu Phe Gln Ala Leu Lys Leu Asn Leu Phe Gly Leu  
 195 200 205  
 80 Val Leu Pro Leu Leu Val Met Ile Ile Cys Tyr Thr Gly Ile Ile Lys  
 210 215 220  
 85 Ile Leu Leu Arg Arg Pro Asn Glu Lys Lys Ser Lys Ala Val Arg Leu  
 225 230 235 240  
 90 Ile Phe Val Ile Met Ile Ile Phe Phe Leu Phe Trp Thr Pro Tyr Asn

245 250 255  
 Leu Thr Ile Leu Ile Ser Val Phe Gln Asp Phe Leu Phe Thr His Glu  
 260 265 270  
 5 Cys Glu Gln Ser Arg His Leu Asp Leu Ala Val Gln Val Thr Glu Val  
 275 280 285  
 10 Ile Ala Tyr Thr His Cys Cys Val Asn Pro Val Ile Tyr Ala Phe Val  
 290 295 300  
 Gly Glu Arg Phe Arg Lys Tyr Leu Arg Gln Leu Phe His Arg Arg Val  
 305 310 315 320  
 15 Ala Val His Leu Val Lys Trp Leu Pro Phe Leu Ser Val Asp Arg Leu  
 325 330 335  
 Glu Arg Val Ser Ser Thr Ser Pro Ser Thr Gly Glu His Glu Leu Ser  
 340 345 350  
 20 Ala Gly Phe  
 355

## (2) INFORMATION FOR SEQ ID NO:14:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 374 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 30 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

40 Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser  
 1 5 10 15  
 Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys  
 20 25 30  
 45 His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu  
 35 40 45  
 Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val  
 50 55 60  
 Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr  
 65 70 75 80  
 55 Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro  
 85 90 95  
 Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met  
 100 105 110  
 60 Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile

	115	120	125
	Phe Phe Ile Ile Leu Leu Thr	Ile Asp Arg Tyr	Leu Ala Ile Val His
	130	135	140
5	Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr	Phe Gly Val Val Thr	
	145	150	155 160
10	Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile		
	165	170	175
	Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro		
	180	185	190
15	Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile		
	195	200	205
	Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly		
	210	215	220
20	Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg		
	225	230	235 240
25	Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp		
	245	250	255
	Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe		
	260	265	270
30	Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln		
	275	280	285
	Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile		
	290	295	300
35	Tyr Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu		
	305	310	315 320
40	Gly Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly		
	325	330	335
	Val Arg Pro Gly Lys Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp		
	340	345	350
45	Gly Arg Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu		
	355	360	365
	Gln Asp Lys Glu Gly Ala		
	370		

50

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: protein

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

5 Met Thr Thr Ser Leu Asp Thr Val Glu Thr Phe Gly Thr Thr Ser Tyr  
1 5 10 15

10 Tyr Asp Asp Val Gly Leu Leu Cys Glu Lys Ala Asp Thr Arg Ala Leu  
20 25 30

Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Val Gly  
35 40 45

15 Leu Leu Gly Asn Val Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg  
50 55 60

Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp  
65 70 75 80

20 Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly  
85 90 95

25 His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly Phe  
100 105 110

Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr  
115 120 125

30 Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala  
130 135 140

Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly Leu  
145 150 155 160

35 Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu  
165 170 175

Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val  
180 185 190

40 Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu  
195 200 205

45 Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys  
210 215 220

Thr Leu Leu Arg Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg Leu  
225 230 235 240

50 Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn  
245 250 255

Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp  
260 265 270

55 Cys Glu Arg Ser Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val  
275 280 285

60 Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val

290 295 300

Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu  
305 310 315 320

5 Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu  
325 330 335

10 Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser  
340 345 350

Ile Val Phe  
355

15 (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 360 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

30 Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr  
1 5 10 15

Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu  
20 25 30

35 Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu  
35 40 45

40 Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu  
50 55 60

Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn  
65 70 75 80

45 Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly  
85 90 95

Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met  
100 105 110

50 Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val  
115 120 125

55 Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe  
130 135 140

Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala  
145 150 155 160

60 Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser

	165	170	175
	Thr Cys Tyr Thr Glu Arg Asn His	Thr Tyr Cys Lys Thr	Lys Tyr Ser
	180	185	190
5	Leu Asn Ser Thr Thr Trp Lys Val	Leu Ser Ser Leu Glu Ile Asn Ile	
	195	200	205
	Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met		
10	210	215	220
	Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala		
	225	230	235
15	Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp Thr		
	245	250	255
	Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val		
20	260	265	270
	Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala		
	275	280	285
	Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr		
25	290	295	300
	Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys		
	305	310	315
30	Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln		
	325	330	335
	Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr Met		
35	340	345	350
	Asp His Asp Leu His Asp Ala Leu		
	355	360	

## (2) INFORMATION FOR SEQ ID NO:17:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

45

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAATGATCA GTCAACGGGG GAC

23

55

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

10

CCAGCAAGCT TGCAACCTTA ACCA

24

(2) INFORMATION FOR SEQ ID NO:19:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: peptide

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asp Tyr Lys Asp Asp Asp Asp Lys Leu  
1 5

30